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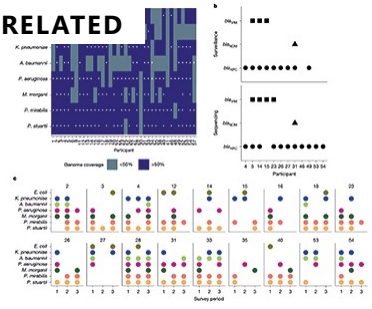
Nursing-home residents' skin is a source of transmitted harmful and drug-resistant microbes

Genomic sequencing has revealed that individual strains of life-threatening, antibiotic-resistant bacteria and *Candida auris* fungi reside on human skin and can be commonly transmitted between residents of nursing homes.

By Teresa R. O'Meara

Candida auris is a fungal species that causes human disease. It was discovered[1] in 2009 and has caused life-threatening and body-wide (systemic) outbreaks of infection in people around the world. This species is unusual among disease-causing fungi in its ability to drive hospital-associated outbreaks. Writing in *Nature*, Proctor *et al.*[2] reveal that *C. auris* is present on the skin and can be spread between individuals in clinical settings such as nursing homes.



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Read the paper: Clonal *Candida auris* and ESKAPE pathogens on the skin of residents of nursing homes

Most invasive fungal infections come from exposure to fungi in the environment, as is the case with fungal infections by species of the *Coccidioides* genus, which causes a condition called valley fever[3]. Some fungal infections can instead arise internally in the body, such as when the normal gut-resident fungus *Candida parapsilosis* moves to the bloodstream to cause infection throughout the body[4]. By contrast, people

generally acquire *C. auris* from exposure in health-care settings, especially in skilled nursing homes where they receive temporary intensive care rather than long-term care, and in the context of long-term acute care in hospitals[5–7]. This pattern of spread is reminiscent of that of common harmful bacteria, especially those described as the ESKAPE pathogens (an abbreviation of the infectious-species names *Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa* and species of the *Enterobacter* genus, including *Escherichia coli*).

Proctor *et al.* used a DNA-sequencing technique to generate genome sequences termed metagenome-assembled genomes (MAGs) to identify the sharing of multiple pathogenic strains between individuals, including multi-drug-resistant bacterial pathogens and *C. auris*. The authors propose that long-term skin colonization by these organisms serves as a source for spread when people move between nursing homes and hospitals. This study presents an alarming picture in which nursing homes are a reservoir for antimicrobial resistance to first-line therapeutics, and strain sharing of these dangerous microorganisms is widespread. Future work on these transmission dynamics will be crucial for developing targeted efforts to prevent infection to avoid spreading these drug-resistant pathogens throughout health-care systems.

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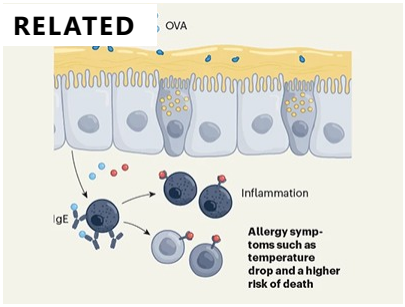

A gut fungus protects mice against parasitic worms but increases allergies

Proctor *et al.* previously observed signs of co-occurrence between *C. auris* and *K. pneumoniae* and *P. aeruginosa*[5], but were unable to resolve whether this was because of strain sharing between individuals. In the standard approach for tracking microbial transmission in clinical settings, microbes are collected from a person, then cultured *in vitro* and sequenced. This is labour-intensive and given that not all microbes are easy to culture successfully, the species that grow

better *in vitro* are more likely to be identified.

To deal with this issue, Proctor *et al*. used a comprehensive form of sequencing (strain-resolved metagenomics) to reconstruct the complete genomes of all of the microbes in the sample. This approach enabled strain identification, including that of multiple strains of the same species from individual people. This information is needed to determine whether specific strains are being shared between people in nursing homes. Furthermore, this approach can determine whether genes enabling characteristics of interest, such as antibiotic resistance, are associated with a specific microbial strain.

The authors swabbed the skin at various body locations (Fig. 1) and sequenced samples taken from 42 individuals over 3 months to generate colonization data over time and space. Proctor and colleagues thereby identified *C. auris* colonization, as well as colonization by at least one ESKAPE pathogen on the skin of most individuals, demonstrating that the skin is a common reservoir for these microbes.

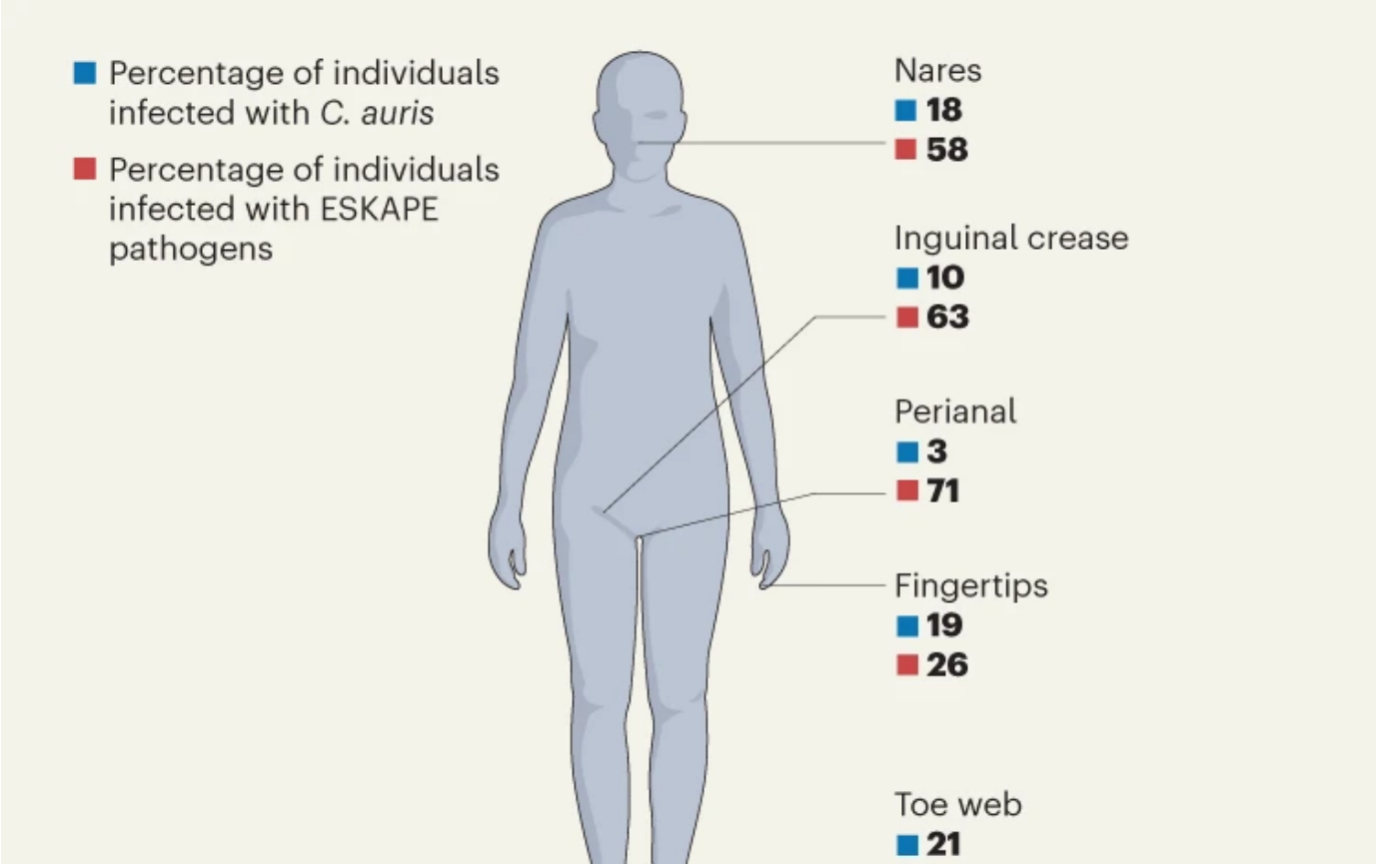

Figure 1 | Harmful microbes found on the skin of residents of nursing homes. Proctor *et al.*[2] assessed the sharing of harmful strains of microbial species for 42 residents of nursing homes. The authors sequenced DNA from skin swabs taken from five sites: the nasal passages (nares); fingertips; inguinal crease (where the lower abdomen meets the inner thigh); perianal skin (skin around the anus); and toe webs, obtaining samples from 40, 42, 40, 38 and 39 out of the 42 residents, for these respective sites. The fungus *Candida auris*, which is potentially life-threatening, was found as well as microbes termed ESKAPE pathogens (data illustrated here for the species *Escherichia coli, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii,* and *Pseudomonas aeruginosa* tallies individuals infected with at least one of these species). Some people whose data is presented here had both *C. auris* and ESKAPE infections (not shown).

The presence of these pathogens was consistently found over the three-month sampling period and can be attributed to either persistent colonization or repeated re-colonization. Evidence for multiple colonization events lies in the identification of some residents with strain replacement or infection with multiple different strains of the same pathogen. In other cases, there was clear domination by a single strain shared between residents. For example, the authors identified spread of a single (clonal) genetic lineage of *C. auris* across multiple facilities in the Chicago metropolitan area, Illinois, and a spread through organ donation from Chicago, resulting in transmission of infection to a person in Massachusetts.

Similarly, by examining publicly available data of metagenome sequence analysis, the authors found evidence suggesting the sharing of ESKAPE strains among residents in different nursing homes. Scientists should also explore whether the non-pathogenic normal bacterial strains (commensals) on the skin are also shared, and if they are, whether the transmission dynamics differ between pathogens and non-pathogens.

A benefit of MAGs is that strain identification can find interesting associations

between microbes. For instance, *C. auris* is frequently found along with *Staphylococcus pettenkoferi* but not found with *P. aeruginosa*. Similarly *C. auris* was not found alongside species of the fungus genus *Malassezia*[5]. Studying the dynamics between different types of microbe at these body sites will be an exciting avenue for future research.

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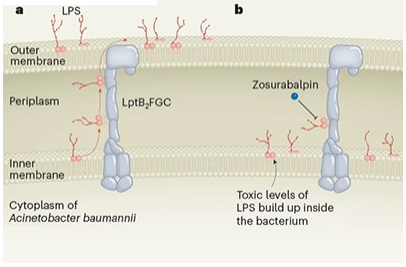

A new type of antibiotic targets a drug-resistant bacterium

The authors observed consistent skin colonization with pathogens, including from species that were not previously known to be associated with the skin. One potential explanation is that, although the presence of the studied microbes is not found when testing stool samples, the microbes might indeed be in the gut and are transported to the perianal area by faecal matter, and then can spread to other skin areas from there. The authors examined the distribution of the 48 most abundant species found in perianal samples. Indeed, the bacteria that do not require oxygen for survival (anaerobes) and can therefore survive in the low-oxygen environment of the gut, were more commonly found in perianal regions and at the nearby inguinal crease, compared with their prevalence at other skin locations. However, microbes that are able to thrive in both low or high levels of oxygen (facultative anaerobes), which include ESKAPE pathogens, were more common on fingertips, toe webs and nostrils (nares) than on the other sites. This suggests that the fingertips, toe webs and nares might act as reservoirs for transmission and are therefore worth including in sampling efforts for surveillance of microbial infection.

On the basis of their sequencing data, the authors identified the presence of genes on the skin that confer resistance to the antibiotic carbapenem. These were present even months after clinical testing initially detected signs of microbes that have this sort of drug resistance. This suggests persistent or repeated colonization by drug-resistant pathogens. This gene signature was all over the body, not just at perianal sites,

suggesting that the skin is a major reservoir of microbes that harbour genes for drug resistance. Further epidemiological analyses are needed to determine whether having this skin reservoir increases the likelihood of a person developing a carbapenem-resistant infection.

Despite the sequence similarity between the clonal strains identified, their clinical characteristics might still be variable. Many of the drug-resistant *C. auris* strains arise because of single nucleotide changes in genes needed to make the molecule ergosterol, a component of the fungal cell membrane. This highlights the consequences of a single-nucleotide mutation on clinical outcomes[8]. Moreover, Proctor and colleagues' analysis focuses on the 'core' genome and did not assess other types of genetic variation, such as the presence or number of circular DNA (plasmids) or variations in the copy number of chromosomes in the *C. auris* MAGs. Even if mutations in the core genome are absent, these other genetic variations might influence strain behaviour.

Future research will undoubtedly focus on understanding genetic variations in strains of species and their effects on microbial characteristics. The high prevalence of *C. auris* and ESKAPE pathogens on the skin of nursing-home residents provides a large reservoir of genetic variation for evolution to act on, increasing the risk of the emergence of dangerous and drug-resistant strains.

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